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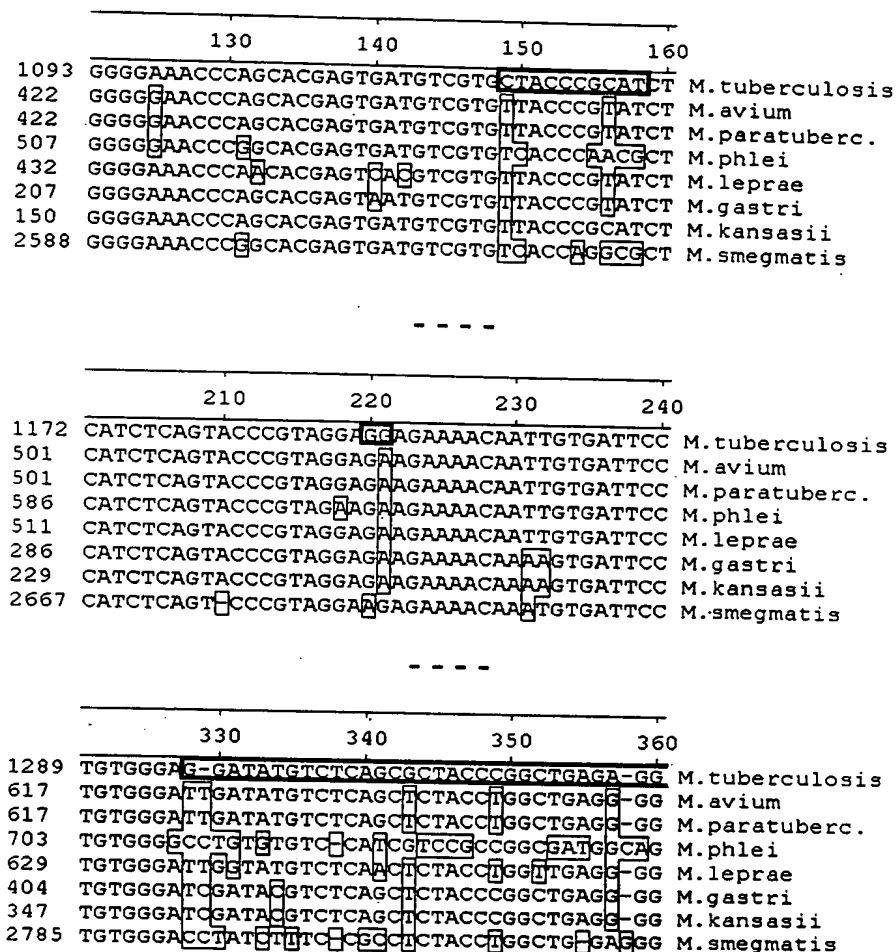


Figure 1A

	370	380	390	400	
1327	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.tuberculosis
656	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.avium
656	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.paratuberc.
742	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.phlei
668	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.leprae
443	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.gastri
386	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.kansasii
2823	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.smegmatis

	450	460	470	480	
1406	CGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.tuberculosis
735	CGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.avium
735	CGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.paratuberc.
820	TGCTGCCGCTGTACAGG--TCCCGAGTAGCAGCGGGCC				M.phlei
747	CGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.leprae
522	CGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.gastri
465	CGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.kansasii
2902	CGACGTCTGCTTATGGTGTTCCTGAGTAGCAGCGGGCC				M.smegmatis
	490	500	510	520	
1446	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.tuberculosis
775	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.avium
775	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.paratuberc.
857	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.phlei
787	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.leprae
562	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.gastri
505	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.kansasii
2942	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.smegmatis

Figure 1B

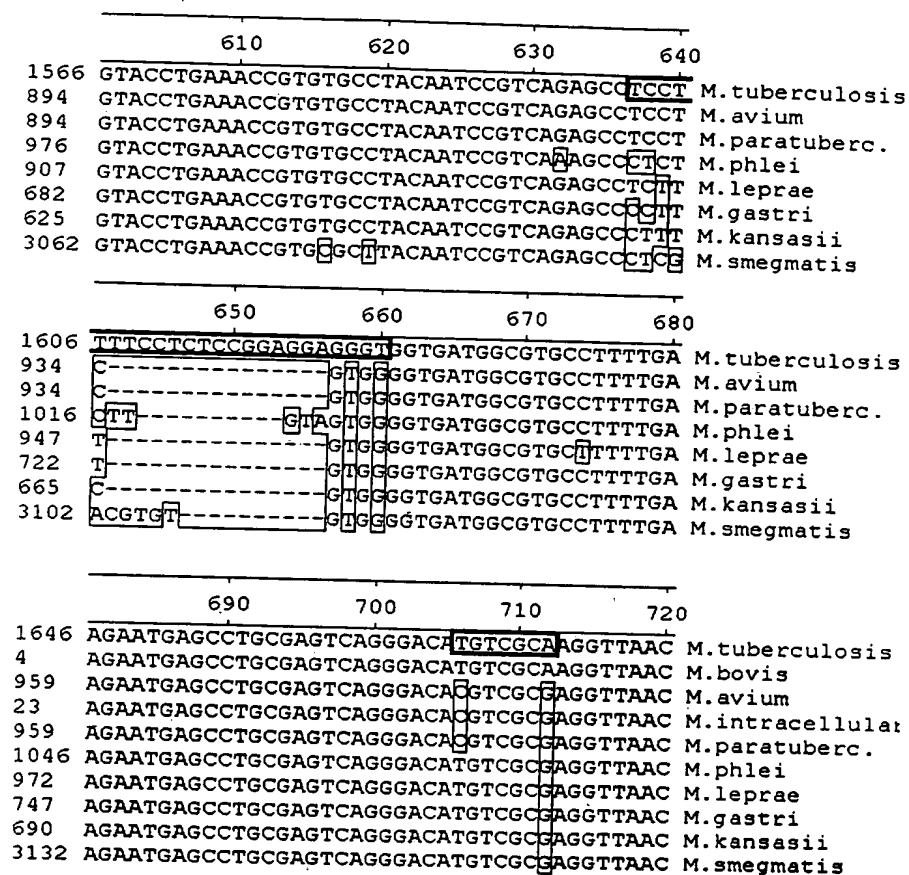


Figure 1C

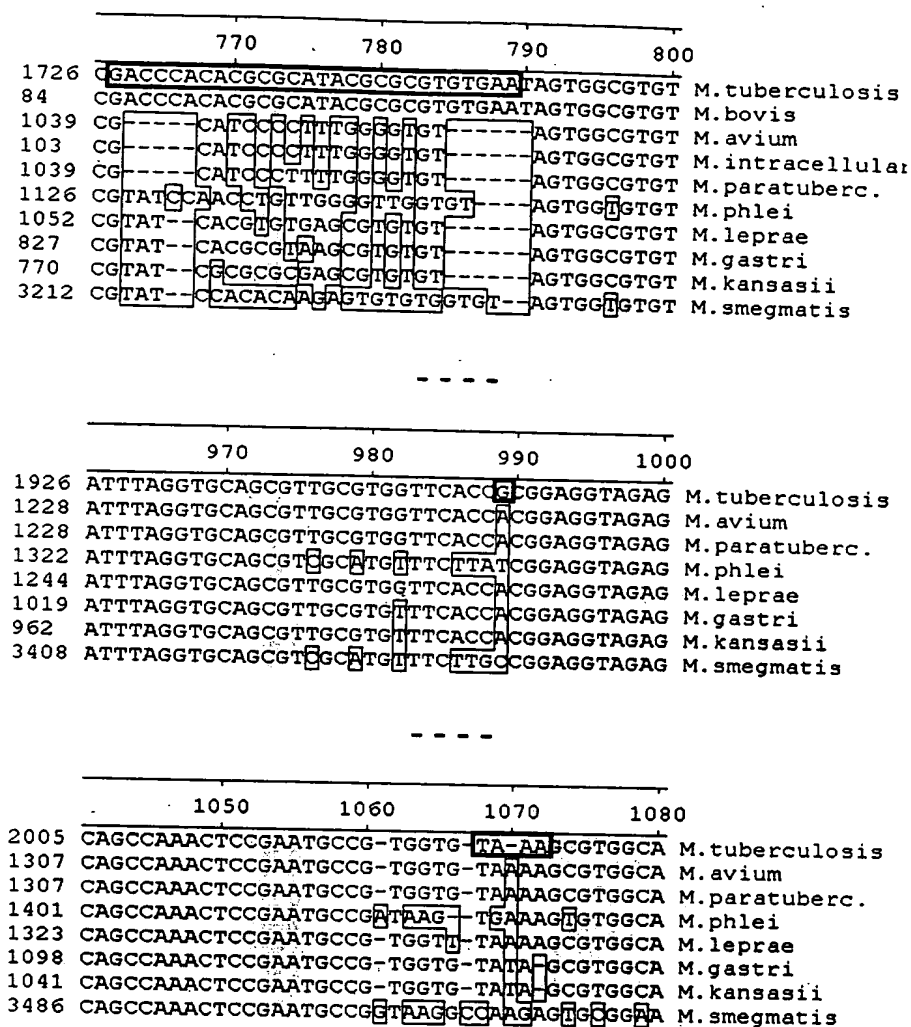


Figure 1D

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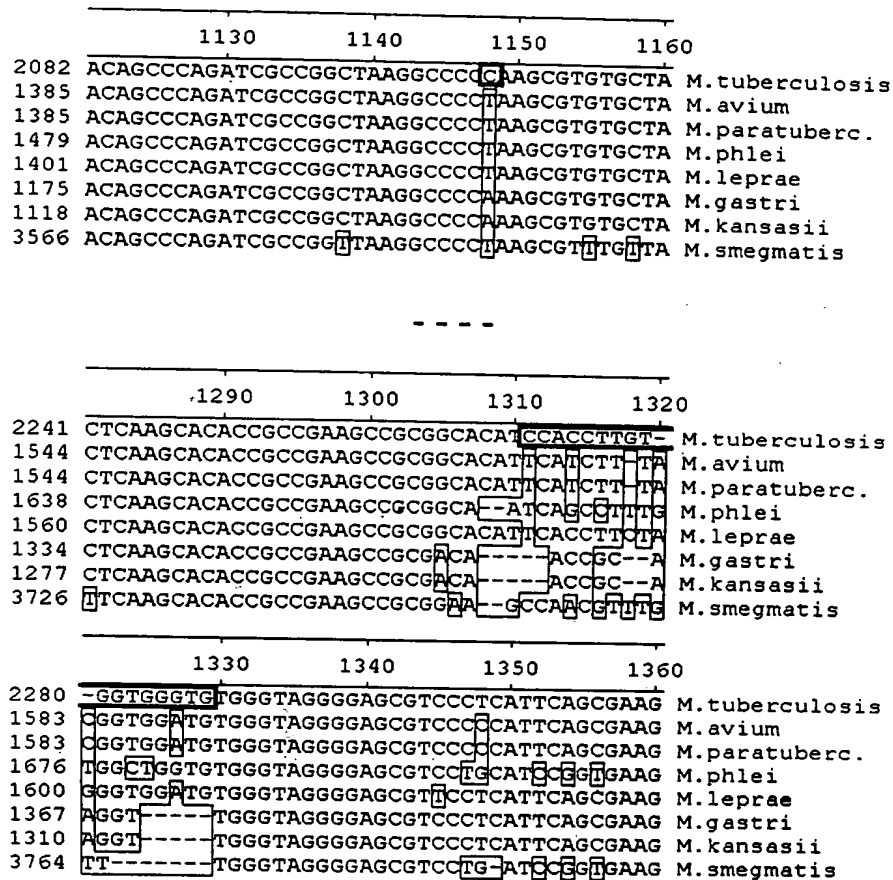


Figure 1E

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	1370	1380	1390	1400	
2319	CCAC	GGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.tuberculosis
1623	CT	CCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.avium
1623	CT	CCGGGTGATCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.paratuberc.
1716	CCGCCG	GTGATCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.phlei
1640	CCGCCG	GTGATCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.leprae
1402	CCGCCG	GTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.gastri
1345	CTGCCG	GTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.kansasii
3796	CCGCCG	GTATCGAGTGGTGGAGGGTGGGGGAGTGAGAAT			M.smegmatis
	1410	1420	1430	1440	
2359	GCAGGCATGAGTAGCGA	CAAGGCAAGTGAGAACCTTGCCC			M.tuberculosis
1662	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.avium
1662	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.paratuberc.
1756	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.phlei
1680	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.leprae
1442	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.gastri
1385	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.kansasii
3836	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.smegmatis
- - - -					
	1570	1580	1590	1600	
2519	CGCCCCGTGAC	BAATCA-GCGGTACTAACCACCCAAAACCG			M.tuberculosis
1821	CGTCCCTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M.avium
1821	CGTCCCTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M.paratuberc.
1915	CGTCCCTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M.phlei
1840	CGCCCCGTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M.leprae
1602	CGCCCCGTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M.gastri
1545	CGCCCCGTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M.kansasii
3996	CGTCCCTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M.smegmatis

Figure 1F

	1610	1620	1630	1640	
2558	GAT-CGATCAC-TCCCCTTCGGGGG	TGTGGAGTTC-TGG			M.tuberculosis
1860	GAT-CGACCAT-TCCCCTTCGGGGG	GTGGCGATT-CGG			M.avium
1860	GAT-CGACCAT-TCCCCTTCGGGGG	GTGGCGATT-CGG			M.paratuberc.
1955	GCG-CGATC-ATCC-TTCGGGG	GTGACGGTTG-GG			M.phlei
1879	GAT-CGACCAT-TCCCCTTCGGGGG	TGTGGAGGTT-CGG			M.leprae
1641	GAT-CGATCAC-TCCCCTTCGGGGG	GTGGAGGTC-TGG			M.gastri
1584	GAT-CGATCAC-TCCCCTTCGGGGG	GTGGAGGTC-TGG			M.kansasii
4035	ACCGTGACCCACCT-TTCGGGG	TGTGGCGTTGGTGG			M.smegmatis

	1650	1660	1670	1680	
2594	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.tuberculosis
1896	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.avium
1896	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.paratuberc.
1986	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.phlei
1917	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.leprae
1677	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.gastri
1620	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.kansasii
4071	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.smegmatis

	1690	1700	1710	1720	
2634	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.tuberculosis
1936	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.avium
1936	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.paratuberc.
2025	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.phlei
1957	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.leprae
1717	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.gastri
1660	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.kansasii
4111	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.smegmatis

Figure 1G

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	1730	1740	1750	1760	
2672	-CTGGGGCAAGCC	GGTAGGG	AGAGCGATAGGCAAATCCGT		M.tuberculosis
1974	-CTGGGGCAAGCC	GTAG--	AGAGCGATAGGCAAATCCGT		M.avium
1974	-CTGGGGCAAGCC	GTAG--	AGAGCGATAGGCAAATCCGT		M.paratuberc.
2063	-C	GGGGTAAACCTGTAGGG	GGAGTGATAGGCAAATCCGT		M.phlei
1995	-CTGGG	AGCAAGCCGTAGGGAGAGCGATAGGCAAATCCGT			M.leprae
1755	-CTGGGGCAAGCC	AGTAGGGAGAGCGATAGGCAAATCCGT			M.gastri
1698	-CTGGGGCAAGCC	AGTAGGGAGAGCGATAGGCAAATCCGT			M.kansasii
4149	-C	GGGGTAAGCCGTAGGGAGTCA	GATAGGTAAATCCGT		M.smegmatis

	1970	1980	1990	2000	
2908	AGGGGG	ACCGGAATATCGTGAACACCC	TTGCGGTGGGAGC		M.tuberculosis
2208	AGGGGG	CCCGGAATACCGTGAACACCC	TTGCGGTGGGAGC		M.avium
2208	AGGGGG	CCCGGAATACCGTGAACACCC	TTGCGGTGGGAGC		M.paratuberc.
2298	AGGGGGACCC	CACGTACCGTGAGGG	CTTGC	GGGGAGC	M.phlei
2231	AGGGGG	CCCGGAATATCGTGAACACCC	TTGCGGTGGGAGC		M.leprae
1910					M.gastri
1934	AGGGGGACCC	GGAATACCGTGAACACCC	TTGCGGTGGGAGC		M.kansasii
4385	AGGGGGACCC	CACATGCGTGTAAGCC	TTACGG	CCCAAGC	M.smegmatis

	2410	2420	2430	2440	
3345	ACCTCGACGCCAGTTGGGGG	CGAGTCGTTGTTGAAATACC			M.tuberculosis
284	ACCTCGACGCCAGTTGGGGG	CGAGTCGTTGTTGAAATACC			M.bovis
2645	GCACAGACGCCAGTTGGTGG	GGAGTCGTTGTTGAAATACC			M.avium
393	ATACAGACGCCAGTTGGTAT	GGAGTCGTTGTTGAAATACC			M.intracellulare
2645	GCACAGACGCCAGTTGGTGG	GGAGTCGTTGTTGAAATACC			M.paratuberc.
2737	GCTCGGACGCCAGTTGGGGT	GGAGTCGTTGTTGAAATACC			M.phlei
2668	ACCTCGACGCC	TAGTTGGGGTGGAGTCGTTGTTGAAATACC			M.leprae
1910					M.gastri
2372	ACCTCGACGCCAGTTGGGGT	GGAGTCGTTGTTGAAATACC			M.kansasii
4822	GCTCAGACGCCAGTTGGGGT	GGAGTCGTTGTTGAAATACC			M.smegmatis

Figure 1H

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	2450	2460	2470	2480	
3385	ACTCTGATCGTATTGG	GCATCTAACCTCGAACCCCTGAATC			M.tuberculosis
324	ACTCTGATCGTATTGGGCATCTAACCTCGAACCCCTGAATC				M.bovis
2685	ACTCTGATCGTATTGG	CACCTAACCTCGAACCCCT-TATC			M.avium
433	ACTCTGATCGTATTGG	CACCTAACCTCGAACCCCT-TATC			M.intracellulare
2685	ACTCTGATCGTATTGG	CACCTAACCTCGAACCCCT-TATC			M.paratuberc.
2777	ACTCTGATCGTATTGGGC	TCTAACCTCGAACCTGATC			M.phlei
2708	ACTCTGAT	GTATTGACATCTAACCTCGAACCTATATC			M.leprae
1910					M.gastri
2412	ACTCTGATCGTATTGG	CACCTAACCTCGAACCCCTGAATC			M.kansasii
4862	ACTCTGATCGTATTGGGC	TCTAACCTCGAACCTATATC			M.smegmatis

	2490	2500	2510	2520	
3425	GGGTTTAG	GGACAGTGCCTGGCGGGTAGTTTAACTGGGGC			M.tuberculosis
364	GGGTTTAGGGACAGTGCCTGGCGGGTAGTTTAACTGGGGC				M.bovis
2724	GGGTTTAGGGACAGTGCCTGGCGGGTAGTTTAACTGGGGC				M.avium
472	GGGTTTAGGGACAGTGCCTGGCGGGTAGTTTAACTGGGGC				M.intracellulare
2724	GGGTTTAGGGACAGTGCCTGGCGGGTAGTTTAACTGGGGC				M.paratuberc.
2817	GGGTTTAGGGACAGTGCCTGG	GGGTAGTTTAACTGGGGC			M.phlei
2748	GGGTTTAGGGACAGTGCCTGGCGGGTAGTTTAACTGGGGC				M.leprae
1910					M.gastri
2452	GGGTTTAGGGACAGTGCCTGGCGGGTAGTTTAACTGGGGC				M.kansasii
4902	GGGTTTAGGGACAGTGCCTGG	GGGTAGTTTAACTGGGGC			M.smegmatis

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	2930	2940	2950	2960	
3864	AGTACGAGAGGACCGGGACGGACGAACCTCT	GGTGACCA			M.tuberculosis
3163	AGTACGAGAGGACCGGGACGGACGAACCTCTGGTATACCA				M.avium
3163	AGTACGAGAGGACCGGGACGGACGAACCTCTGGTATACCA				M.paratuberc.
3256	AGTACGAGAGGACCGGGACGGACGAACCTCTGGTATACCA				M.phlei
3187	AGTACGAGAGGACCGGGACGGACGAACCTCTGGTATACCA				M.leprae
1910					M.gastri
2891	AGTACGAGAGGACCGGGACGGACGAACCTCT	GTGCACCA			M.kansasii
5342	AGTACGAGAGGACCGGGACGGACGAACCTCTGGTATACCA				M.smegmatis

Figure 11

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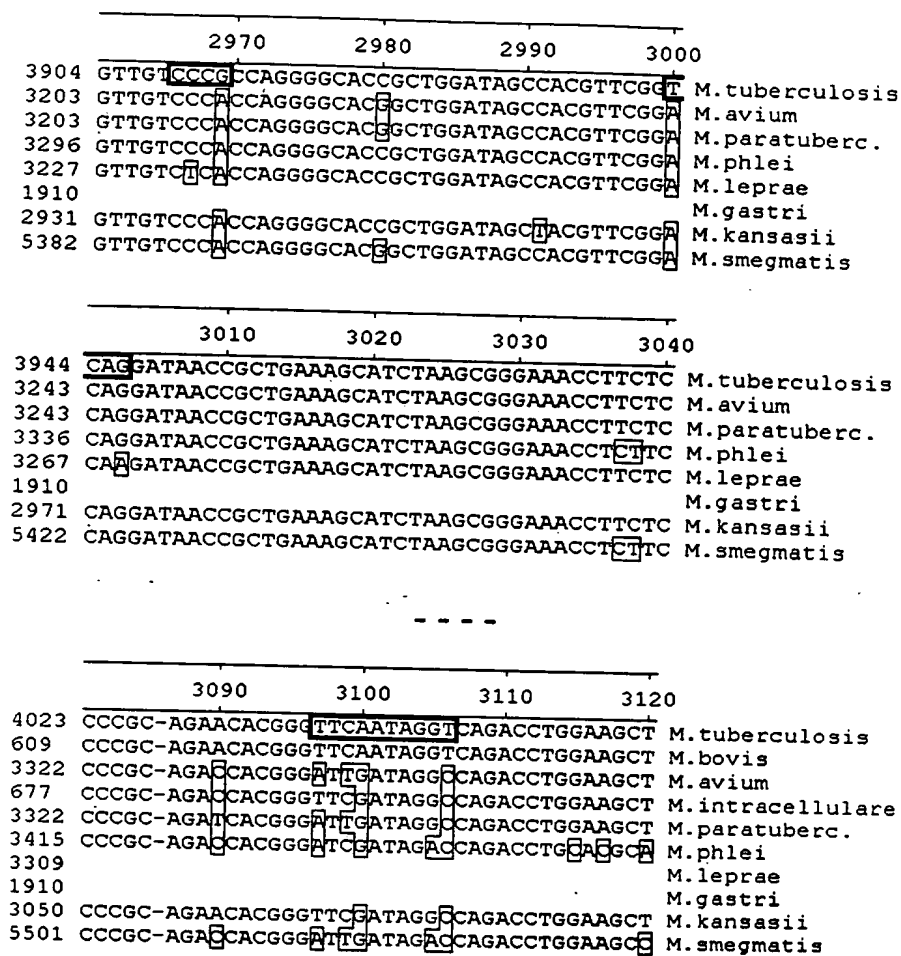


Figure 1J

	50	60	70	80	
2	GCGGCGTGCTTAAACATGCAAGTCGAACGGAAGG	GTCTC			M.tuberculosis
141	GCGGCGTGCTTAAACATGCAAGTCGAACGGAAGG	GTCTC			M.bovis
39	GCGGCGTGCTTAAACATGCAAGTCGAACGGAAGG	GTCTC			M.avium
1	-----TTAAACATGCAAGTCGAACGGAAGG	GTCTC			M.intracellulare
39	GCGGCGTGCTTAAACATGCAAGTCGAACGGAAGG	GTCTC			M.paratuberc.
2	GCGGCGTGCTTAAACATGCAAGTCGAACGGAAGG	GTCTC			M.scrofulaceum
40	GCGGCGTGCTTAAACATGCAAGTCGAACGGAAGG	GTCTC			M.leprae
2	CGGCGTGCTTAAACATGCAAGTCGAACGGAAGG	GTCTC			M.kansasii
2	GCGGCGTGCTTAAACATGCAAGTCGAACGGAAGG	GTCTC			M.gastri
40	GCGGCGTGCTTAAACATGCAAGTCGAACGGAAGG	GTCTC			M.gordonae
1	-----GTGCTTAAACATGCAAGTCGAACGGAAGG	GTCTC			M.marinum

	90	100	110	120	
42	T-----TCGGAGATCTCGAGTGGCGAACGGGT				M.tuberculosis
181	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.bovis
79	T-----TCGGAGTACTCGAGTGGCGAACGGGT				M.avium
32	T-----TCGGGGTACTCGAGTGGCGAACGGGT				M.intracellulare
79	T-----TCGGAGTACTCGAGTGGCGAACGGGT				M.paratuberc.
42	T-----TCGGGGTACTCGAGTGGCGAACGGGT				M.scrofulaceum
80	TAAAAAATCTTTTATAGAGATACTCGAGTGGCGAACGGGT				M.leprae
41	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.kansasii
42	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.gastri
80	-----GGGGTACTCGAGTGGCGAACGGGT				M.gordonae
36	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.marinum

	130	140	150	160	
70	GAGTAACACGTGGGTGATCTGCCCTGCACTTC	GGGATAA			M.tuberculosis
209	GAGTAACACGTGGGTGATCTGCCCTGCACTTC	GGGATAA			M.bovis
107	GAGTAACACGTGGGTGATCTGCCCTGCACTTC	GGGATAA			M.avium
59	GAGTAACACGTGGGTGATCTGCCCTGCACTTC	GGGATAA			M.intracellulare
107	GAGTAACACGTGGGTGATCTGCCCTGCACTTC	GGGATAA			M.paratuberc.
70	GAGTAACACGTGGGTGATCTGCCCTGCACTTC	GGGATAA			M.scrofulaceum
120	GAGTAACACGTGGGTGATCTGCCCTGCACTTC	GGGATAA			M.leprae
69	GAGTAACACGTGGGTGATCTGCCCTGCACTTC	GGGATAA			M.kansasii
70	GAGTAACACGTGGGTGATCTGCCCTGCACTTC	GGGATAA			M.gastri
104	GAGTAACACGTGGGTGATCTGCCCTGCACTTC	GGGATAA			M.gordonae
64	GAGTAACACGTGGGTGATCTGCCCTGCACTTC	GGGATAA			M.marinum

Figure 2A

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	170	180	190	200	
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGAC	CACGGGA			M.tuberculosis
248	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M.bovis
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTCAAGA				M.avium
98	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTTAGG				M.intracellulare
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTCAAGA				M.paratuberc.
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACTTGG				M.scrofulaceum
160	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTCAAGA				M.leprae
108	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACTTGG				M.kansasii
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACTTGG				M.gastri
143	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACTTGG				M.gordonae
103	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M.marinum

	210	220	230	240	
149	TGCATGTCTTGTGGTGGAAAG	CGCTTTAG	CGGTGTGGGAT		M.tuberculosis
288	TGCATGTCTTGTGGTGGAAAGCGCTTTAGCGGTGTGGGAT				M.bovis
186	CGCATGTCTTGTGGTGGAAAGC	TTTT	ACGGTGTGGGAT		M.avium
138	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.intracellulare
186	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.paratuberc.
149	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.scrofulaceum
200	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.leprae
148	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.kansasii
149	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.gastri
183	CACATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.gordonae
143	TTCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.marinum

	250	260	270	280	
189	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.tuberculosis
328	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.bovis
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.avium
176	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.intracellulare
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.paratuberc.
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.scrofulaceum
239	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.leprae
186	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.kansasii
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.gastri
221	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.gordonae
181	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.marinum

Figure 2B

	450	460	470	480	
389	AAACCTCTTTTACCATCGACGAAGGTCCGGGTT				M.tuberculosis
528	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG				M.bovis
424	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTTCTCTCGG				M.avium
376	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTTCTCTCGG				M.intracellulare
424	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTTCTCTCGG				M.paratuberc.
387	AAACCTCTTTTACCATCGACGAAGGTCTCA---CTTGTGG				M.scrofulaceum
439	AAACCTCTTTTACCATCGACGAAGGTCTGGGAATCTCTCGG				M.leprae
386	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCTCGG				M.kansasii
387	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTTCTCTCGG				M.gastri
420	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTTCTCTCGG				M.gordonae
381	AAACCTCTTTTACCATCGACGAAGGTCTGGGTTTCTCTCGG				M.marinum

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	1130	1140	1150	1160	
1069	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.tuberculosis
1208	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.bovis
1104	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.avium
1056	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.intracellulare
1098	TCTCATGTTGCCAGCGGGTAATGCCAGGGGACTCGTGAGAG				M.paratuberc.
1064	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.scrofulaceum
1119	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.leprae
1066	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.kansasii
1067	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gastri
1100	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gordonae
1061	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.marinum

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	1250	1260	1270	1280	
1189	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.tuberculosis
1328	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.bovis
1224	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.avium
1176	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.intracellulare
1218	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.paratuberc.
1184	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.scrofulaceum
1239	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.leprae
1186	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.kansasii
1187	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.gastri
1220	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.gordonae
1181	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.marinum

Figure 2C

	1290	1300	1310	1320	
1229	CGAATCCTTA- A AGCCGGTCTCAGTTCGGAT C GGGTCT				<i>M. tuberculosis</i>
1368	CGAATCCTTA-AAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. bovis</i>
1264	CGAATCCTTTTAAAGCCGG A CTCAGTTCGGAT T GGGGTCT				<i>M. avium</i>
1216	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGAT T GGGGTCT				<i>M. intracellulare</i>
1258	CGAATCCTTTTAAAGCCGG A CTCAGTTCGGAT T GGGGTCT				<i>M. paratuberc.</i>
1224	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. scrofulaceum</i>
1279	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. leprae</i>
1226	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. kansasii</i>
1227	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. gastri</i>
1260	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. gordonae</i>
1221	CGAATCCTTT A -AAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. marinum</i>

	1330	1340	1350	1360	
1268	GCAACTCGACCC G TGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. tuberculosis</i>
1407	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. bovis</i>
1304	GCAACTCGACCC A TGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. avium</i>
1256	GCAACTCGACCC A TGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. intracellulare</i>
1298	GCAACT T GACCC A TGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. paratuberc.</i>
1264	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. scrofulaceum</i>
1319	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. leprae</i>
1266	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. kansasii</i>
1267	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. gastri</i>
1300	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. gordonae</i>
1260	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. marinum</i>

Figure 2D

	50	60	70	80	
128	TTCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC				M.tuberculosis
39	TGCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC				M.bovis
41	TGCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC				M.phlei
3559	TGCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC				M.leprae
5743	TGCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC				M.smegmatis
	90	100	110	120	
168	TGCCCTCCCGGG---TGGAAAAGTAGGACACCGCCGAAC				M.tuberculosis
79	TGCCCTCCCGGG---TGGAAAAGTAGGACACCGCCGAAC				M.bovis
81	TGCCCTCCCGGG---TGGAAAAGTAGGACACCGCCGAAC				M.phlei
3599	TGCCCTCCCGGG---TGGAAAAGTAGGACACCGCCGAAC				M.leprae
5782	TGCCCTCCCGGG---TGGAAAAGTAGGACACCGCCGAAC				M.smegmatis

Figure 3

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	90	100	110	120	
382	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATTTCCGAAT			M.avium
382	GGGAGCTGTCAACCGAGCATTGATCCGAGGATTTCCGAAT				M.paratuberc.
1053	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.tuberculosis
467	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.phlei
392	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.leprae
167	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.gastri
110	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.kansasii
2548	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.smegmatis

	170	180	190	200	
462	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.avium
462	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.paratuberc.
1133	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.tuberculosis
547	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.phlei
472	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.leprae
247	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.gastri
190	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.kansasii
2628	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.smegmatis

	250	260	270	280	
541	-GTCAGTAGTGGCGAGCGAAC	CGGAACA-GGCTAAACCG			M.avium
541	-GTCAGTAGTGGCGAGCGAAC	CGGAACA-GGCTAAACCG			M.paratuberc.
1212	-GTCAGTAGTGGCGAGCGAAC	CGGAACA-GGCTAAACCG			M.tuberculosis
626	-GTCAGTAGTGGCGAGCGAAC	CGGAACA-GGCTAAACCG			M.phlei
551	-GTCAGTAGTGGCGAGCGAAC	CGGAACA-GGCTAAACCG			M.leprae
326	-GTCAGTAGTGGCGAGCGAAC	CGGAACA-GGCTAAACCG			M.gastri
269	-GTCAGTAGTGGCGAGCGAAC	CGGAACA-GGCTAAACCG			M.kansasii
2706	-GTCAGTAGTGGCGAGCGAAC	CGGAACA-GGCTAAACCG			M.smegmatis

Figure 4A

	290	300	310	320	
578	CATG	CATG	GACA	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. avium
578	CATG	CATG	GACA	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. paratuberc.
1250	CATG	CATG	GTA	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. tuberculosis
664	CATG	CATG	TGATA	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. phlei
590	CACA	CATG	TCT	AACTAGGTAGGGGTTGTGTGTGCGGGGT	M. leprae
365	CACG	CATG	GTG	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. gastri
308	CACG	CATG	GTG	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. kansasii
2745	TATGA	CATG	TGATA	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. smegmatis

	330	340	350	360	
617	TGTGGG	ATTGATATG	TCTCAG	TCTACCTGGCTGAGG	M. avium
617	TGTGGG	ATTGATATG	TCTCAG	TCTACCTGGCTGAGG	M. paratuberc.
1289	TGTGGG	AG	GATATGTCTCAG	TCTACCTGGCTGAGG	M. tuberculosis
703	TGTGGG	SCCTGT	TGTCTCAG	TCTACCTGGCTGAGG	M. phlei
629	TGTGGG	ATTG	TATGTCTCAG	TCTACCTGGCTGAGG	M. leprae
404	TGTGGG	AT	GATATGTCTCAG	TCTACCTGGCTGAGG	M. gastri
347	TGTGGG	AT	GATATGTCTCAG	TCTACCTGGCTGAGG	M. kansasii
2785	TGTGGG	AT	GATATGTCTCAG	TCTACCTGGCTGAGG	M. smegmatis

	370	380	390	400	
656	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGGAT			M. avium
656	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGGAT			M. paratuberc.
1327	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGGAT			M. tuberculosis
742	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGGAT			M. phlei
668	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGGAT			M. leprae
443	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGGAT			M. gastri
386	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGGAT			M. kansasii
2823	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGGAT			M. smegmatis

Figure 4B

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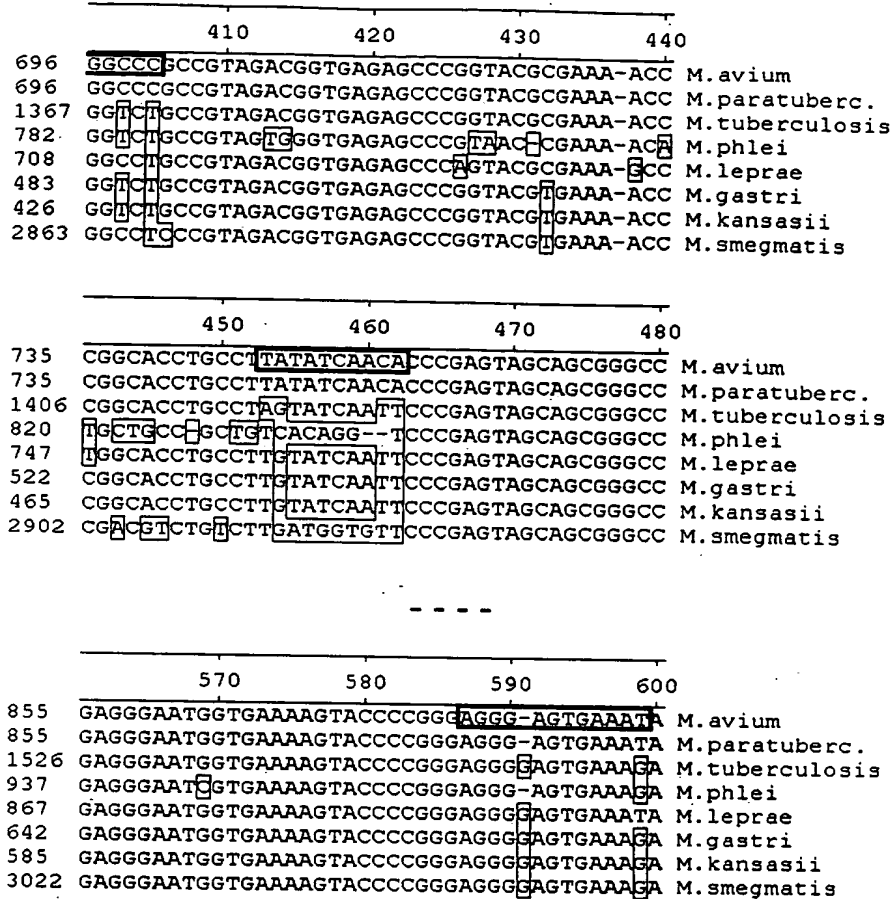


Figure 4C

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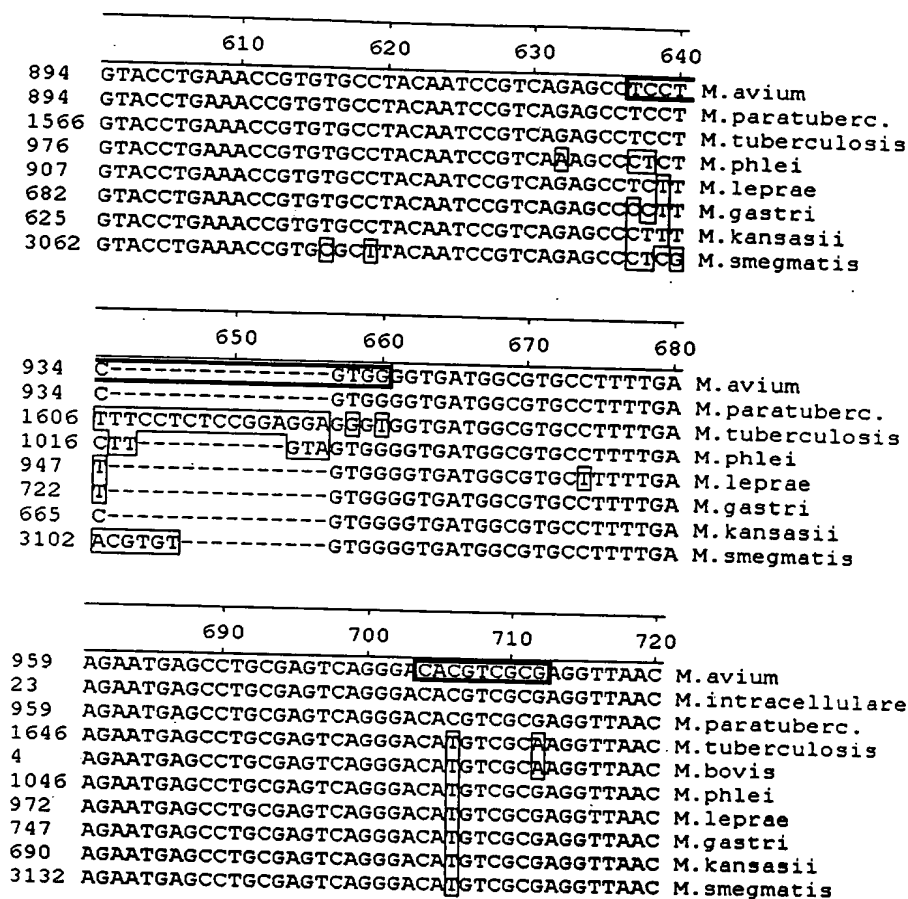


Figure 4D

	770	780	790	800	
1039	CGCATCCCCCTTGGG	-----	GTGTAGTGGCGTGT		M. avium
103	CGCATCCCCCTTGGG	-----	GTGTAGTGGCGTGT		M. intracellulare
1039	CGCATCCCCCTTGGG	-----	GTGTAGTGGCGTGT		M. paratuberc.
1726	CGACCCACACGCGCATACGCGCGTGTGA	TTAGTGGCGTGT			M. tuberculosis
84	CGACCCACACGCGCATACGCGCGTGTGA	TTAGTGGCGTGT			M. bovis
1126	CGTATCCCAACCTGTT	-----	GGGGTTGGTGTAGTGGCGTGT		M. phlei
1052	CGTATCCCAACCTGTT	-----	GGGGTTGGTGTAGTGGCGTGT		M. leprae
827	CGTATCCCAACCTGTT	-----	GGGGTTGGTGTAGTGGCGTGT		M. gastri
770	CGTATCCCAACCTGTT	-----	GGGGTTGGTGTAGTGGCGTGT		M. kansasii
3212	CGTATCCCAACCTGTT	-----	GGGGTTGGTGTAGTGGCGTGT		M. smegmatis

	1050	1060	1070	1080	
1307	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCG	TTGGCA		M. avium
1307	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCG	TTGGCA		M. paratuberc.
2005	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCG	TTGGCA		M. tuberculosis
1401	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCG	TTGGCA		M. phlei
1323	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCG	TTGGCA		M. leprae
1098	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCG	TTGGCA		M. gastri
1041	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCG	TTGGCA		M. kansasii
3486	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCG	TTGGCA		M. smegmatis

	1170	1180	1190	1200	
1425	AGTGGAAAAGGATGTGTAGTCGCAGA	-GACAACCAGGAGG			M. avium
1425	AGTGGAAAAGGATGTGTAGTCGCAGA	-GACAACCAGGAGG			M. paratuberc.
2122	AGTGGAAAAGGATGTGTAGTCGCAGA	-GACAACCAGGAGG			M. tuberculosis
1519	AGTGGAAAAGGATGTGTAGTCGCAGA	-GACAACCAGGAGG			M. phlei
1441	AGTGGAAAAGGATGTGTAGTCGCAGA	-GACAACCAGGAGG			M. leprae
1215	AGTGGAAAAGGATGTGTAGTCGCAGA	-GACAACCAGGAGG			M. gastri
1158	AGTGGAAAAGGATGTGTAGTCGCAGA	-GACAACCAGGAGG			M. kansasii
3606	AGTGGAAAAGGATGTGTAGTCGCAGA	-GACAACCAGGAGG			M. smegmatis

Figure 4E

	1250	1260	1270	1280	
1504	CTCACTGGTCAAGTGATT	ATGCGCC	GATAATGTAGCGGGG		M.avium
1504	CTCACTGGTCAAGTGATT	ATGCGCCGATAATGTAGCGGGG			M.paratuberc.
2201	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M.tuberculosis
1598	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M.phlei
1520	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M.leprae
1294	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M.gastri
1237	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M.kansasii
3686	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M.smegmatis

	1290	1300	1310	1320	
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.avium
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.paratuberc.
2241	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CACTTGT			M.tuberculosis
1638	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CACTTGT			M.phlei
1560	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CACTTGT			M.leprae
1334	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CACTTGT			M.gastri
1277	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CACTTGT			M.kansasii
3726	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CACTTGT			M.smegmatis

	1330	1340	1350	1360	
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.avium
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.paratuberc.
2280	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.tuberculosis
1676	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.phlei
1600	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.leprae
1367	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.gastri
1310	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.kansasii
3764	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.smegmatis

Figure 4F

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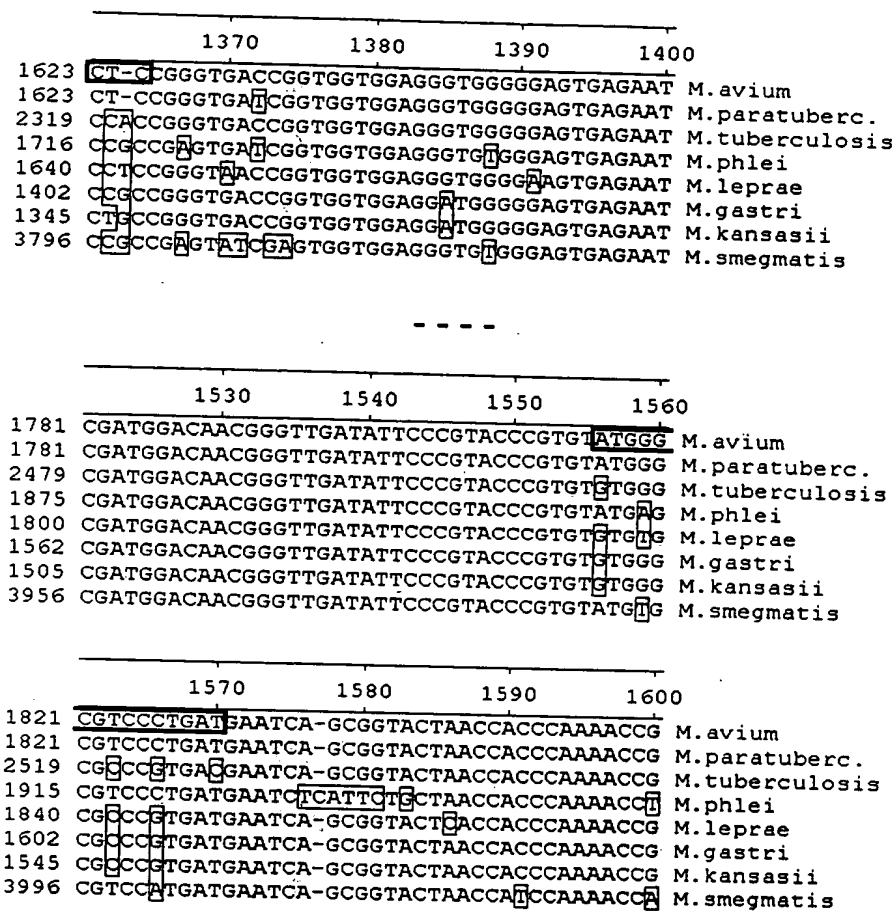


Figure 4G

	1610	1620	1630	1640	
1860	GAT-CGATCCAT-TCCCTTCGGGGG	C-GTGGCGATT-CGG			M. avium
1860	GAT-CGACCAT-TCCCCTTCGGGGG	C-GTGGCGATT-CGG			M. paratuberc.
2558	GAT-CGATCAC-TCCCCTTCGGGGG	TGTGGAGTTG-TGG			M. tuberculosis
1955	GCG-CGATC-ATCC-TTCGGGG	-GTGGCGTTG-GG			M. phlei
1879	GAT-CGACCATA-TCCCCTTCGGGGG	CTATGGAGTT-CGG			M. leprae
1641	GAT-CGATCAC-TCCCCTTCGGGGG	-GTGGAGTTG-TGG			M. gastri
1584	GAT-CGATCAC-TCCCCTTCGGGGG	-GTGGAGTTG-TGG			M. kansasii
4035	ACCGTGACCGACCT-TTCGGGG	-TGTGGCGTTGGTGG			M. smegmatis

	1650	1660	1670	1680	
1896	GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAG	CAATGGG			M. avium
1896	GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAG	CAATGGG			M. paratuberc.
2594	GGCTGCGTGGGAACTTCGCTGGTAGTAGTCAAG	CAATGGG			M. tuberculosis
1986	GGCTGCGTGGGACCG-GTGGTAGTAGTCAAGCAATGGG				M. phlei
1917	GGCTGCGTGGGAACTTCGCTGGTAGTAGTCAAG	CAATGGG			M. leprae
1677	GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAG	CAATGGG			M. gastri
1620	GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAG	CAATGGG			M. kansasii
4071	GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAG	CAATGGG			M. smegmatis

	1690	1700	1710	1720	
1936	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. avium
1936	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. paratuberc.
2634	-GTGACGCAGGAAGGATAGCCGTACCAGTCAGTGGTAATA-				M. tuberculosis
2025	-GTGACGCAGGAAGGATAGCCGTACCAGTCAGTGGTAATA-				M. phlei
1957	-GTGACGCAGGAAGGATAGCCGTACCAGTCAGTGGTAATA-				M. leprae
1717	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. gastri
1660	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. kansasii
4111	-GTGACGCAGGAAGGATAGCCGTACCAGTCAGTGGTAATA-				M. smegmatis

	1730	1740	1750	1760	
1974	-CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAAATCCGT				M. avium
1974	-CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAAATCCGT				M. paratuberc.
2672	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAAATCCGT				M. tuberculosis
2063	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAAATCCGT				M. phlei
1995	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAAATCCGT				M. leprae
1755	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAAATCCGT				M. gastri
1698	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAAATCCGT				M. kansasii
4149	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAAATCCGT				M. smegmatis

Figure 4H

	1810	1820	1830	1840	
2051	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. avium
2051	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. paratuberc.
2751	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. tuberculosis
2141	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. phlei
2074	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. leprae
1834	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. gastri
1777	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. kansasii
4228	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. smegmatis
	1850	1860	1870	1880	
2089	GCGAGC	ACATACGCGCCCGTACCCCAAACCAACACAGGT			M. avium
2089	GCGAGC	ACATACGCGCCCGTACCCCAAACCAACACAGGT			M. paratuberc.
2789	GCGAGC	ACATACGCGCCCGTACCCCAAACCAACACAGGT			M. tuberculosis
2179	GCGAGC	ACATACGCGCCCGTACCCCAAACCAACACAGGT			M. phlei
2112	GCGAGC	ACATACGCGCCCGTACCCCAAACCAACACAGGT			M. leprae
1872	GCGAGC	ACATACGCGCCCGTACCCCAAACCAACACAGGT			M. gastri
1815	GCGAGC	ACATACGCGCCCGTACCCCAAACCAACACAGGT			M. kansasii
4266	GCGAGC	ACATACGCGCCCGTACCCCAAACCAACACAGGT			M. smegmatis

	1970	1980	1990	2000	
2208	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. avium
2208	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. paratuberc.
2908	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. tuberculosis
2298	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. phlei
2231	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. leprae
1910					M. gastri
1934	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. kansasii
4385	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. smegmatis
	2010	2020	2030	2040	
2248	GGGAT	TCGGTGCAGAAACCAAGTGAGGAGCGACT-GTTTA			M. avium
2248	GGGAT	TCGGTGCAGAAACCAAGTGAGGAGCGACT-GTTTA			M. paratuberc.
2948	GGGAT	TCGGTGCAGAAACCAAGTGAGGAGCGACT-GTTTA			M. tuberculosis
2338	GGGAT	TCGGTGCAGAAACCAAGTGAGGAGCGACT-GTTTA			M. phlei
2271	GGGAT	TCGGTGCAGAAACCAAGTGAGGAGCGACT-GTTTA			M. leprae
1910					M. gastri
1974	GGGAT	TCGGTGCAGAAACCAAGTGAGGAGCGACT-GTTTA			M. kansasii
4425	GGGAT	TCGGTGCAGAAACCAAGTGAGGAGCGACT-GTTTA			M. smegmatis

Figure 4I

	2130	2140	2150	2160	
2367	CCGTTAACC	GT--AAGGGTGAAGCGGAGAATTTAAGCCC			M.avium
2367	CCGTTAACC	CGT--AAGGGTGAAGCGGAGAATTTAAGCCC			M.paratuberc.
3067	CCGTTAACC	CG--AAGGGTGAAGCGGAGAATTTAAGCCC			M.tuberculosis
2457	CCGTTAACC	CTTCGGGGTGAAGCGGAGAATTTAAGCCC			M.phlei
2390	CTGTTAACC	CGA--AAGGGTGAAGCGGAGAATTTAAGCCC			M.leprae
1910					M.gastri
2094	CCGTTAACC	CG--AAGGGTGAAGCGGAGAATTTAAGCCC			M.kansasii
4544	CCGTTAACC	CTTGGGGTGAAGCGGAGAATTTAAGCCC			M.smegmatis

	2250	2260	2270	2280	
2485	GTAACGACTTC	CCAA--TGCTCTCAACCATAGACTCGGCGAA			M.avium
2485	GTAACGACTTC	CGAACTGTCTCAACCATAGACTCGGCGAA			M.paratuberc.
3185	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.tuberculosis
2577	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.phlei
2508	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.leprae
1910					M.gastri
2212	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.kansasii
4663	GTAACGACTTC	CAACTGTCTCAAC--ATAGACTCGGCGAA			M.smegmatis

	2370	2380	2390	2400	
2605	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.avium
2605	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.paratuberc.
3305	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.tuberculosis
2697	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.phlei
2628	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.leprae
1910					M.gastri
2332	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.kansasii
4782	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.smegmatis

Figure 4J

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	2410	2420	2430	2440	
2645	GCACGACGCCAGTTTGTGTTGGAGTCGTTGTTGAAATACC				M. avium
393	ATACAGACGCCAGTTTGTGTTGGAGTCGTTGTTGAAATACC				M. intracellulare
2645	GCACGACGCCAGTTTGTGTTGGAGTCGTTGTTGAAATACC				M. paratuberc.
3345	ACCTCGACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. tuberculosis
284	ACCTCGACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. bovis
2737	GCTCGACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. phlei
2668	ACCTCGACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. leprae
1910					M. gastri
2372	ACCTCAACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. kansasii
4822	GCTCAACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. smegmatis
	2450	2460	2470	2480	
2685	ACTCTGATCGTATTGGACACCTAACGTCGAACCT-TATC				M. avium
433	ACTCTGATCGTATTGGACACCTAACGTCGAACCT-TATC				M. intracellulare
2685	ACTCTGATCGTATTGGACACCTAACGTCGAACCT-TATC				M. paratuberc.
3385	ACTCTGATCGTATTGGGCACTTAACCTCGAACCTGATC				M. tuberculosis
324	ACTCTGATCGTATTGGGCACTTAACCTCGAACCTGATC				M. bovis
2777	ACTCTGATCGTATTGGGCACTTAACCTCGAACCTGATC				M. phlei
2708	ACTCTGATCGTATTGGGCACTTAACCTCGAACCTGATC				M. leprae
1910					M. gastri
2412	ACTCTGATCGTATTGGACACCTAACGTCGAACCTGATC				M. kansasii
4862	ACTCTGATCGTATTGGGCACTTAACCTCGAACCTGATC				M. smegmatis
- - - -					
	2690	2700	2710	2720	
2924	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. avium
2924	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. paratuberc.
3625	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. tuberculosis
3017	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. phlei
2948	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. leprae
1910					M. gastri
2652	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. kansasii
5102	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. smegmatis
	2730	2740	2750	2760	
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. avium
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. paratuberc.
3665	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. tuberculosis
3057	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. phlei
2988	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. leprae
1910					M. gastri
2692	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. kansasii
5142	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. smegmatis

Figure 4K

27/31

	2770	2780	2790	2800	
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. avium
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. paratuberc.
3705	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. tuberculosis
3097	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. phlei
3028	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. leprae
1910					M. gastri
2732	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. kansasii
5182	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. smegmatis
	2810	2820	2830	2840	
3044	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. avium
3044	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. paratuberc.
3745	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. tuberculosis
3137	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. phlei
3068	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. leprae
1910					M. gastri
2772	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. kansasii
5222	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. smegmatis
- - - -					
	3050	3060	3070	3080	
3283	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. avium
638	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. intracellulare
3283	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. paratuberc.
3984	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. tuberculosis
570	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. bovis
3376	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. phlei
3307	CAA				M. leprae
1910					M. gastri
3011	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. kansasii
5462	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. smegmatis
	3090	3100	3110	3120	
3322	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. avium
677	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. intracellulare
3322	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. paratuberc.
4023	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. tuberculosis
609	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. bovis
3415	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. phlei
3309					M. leprae
1910					M. gastri
3050	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. kansasii
5501	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. smegmatis

Figure 4L

	130	140	150	160	
107	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.avium
59	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.intracellulare
107	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.paratuberc.
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.scrofulaceum
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.tuberculosis
209	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.bovis
120	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.leprae
69	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.kansasii
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.gastri
104	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.gordonae
64	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.marinum

	450	460	470	480	
424	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCGG	M.avium
376	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCGG	M.intracellulare
424	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCGG	M.paratuberc.
387	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCGG	M.scrofulaceum
389	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCGG	M.tuberculosis
528	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCGG	M.bovis
439	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCGG	M.leprae
386	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCGG	M.kansasii
387	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCGG	M.gastri
420	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCGG	M.gordonae
381	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCGG	M.marinum
	490	500	510	520	
429	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.tuberculosis
568	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.bovis
464	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.avium
416	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.intracellulare
464	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.paratuberc.
424	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.scrofulaceum
479	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.leprae
426	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.kansasii
427	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.gastri
460	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.gordonae
421	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.marinum

Figure 5A

29/31

	1130	1140	1150	1160	
1104	TCTCATGTTGCCAGC	GGGTAATGC	GGGGACTCGTGAGAG		M.avium
1056	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.intracellulare
1098	TCTCATGTTGCCAGCGGGTAATGC	GGGGACTCGTGAGAG			M.paratuberc.
1064	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.scrofulaceum
1069	TCTCATGTTGCCAGCAGTAATG	GGGGACTCGTGAGAG			M.tuberculosis
1208	TCTCATGTTGCCAGCAGTAATG	GGGGACTCGTGAGAG			M.bovis
1119	TCTCATGTTGCCAGCAGTAATG	GGGGACTCGTGAGAG			M.leprae
1066	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.kansasii
1067	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gastri
1100	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gordonae
1061	TCTCATGTTGCCAGCAGTAATG	GGGGACTCGTGAGAG			M.marinum

- - - -

	1290	1300	1310	1320	
1264	CGAATCCTTTTAAGCCGGACTCAGTTCGGAT	GGGGTCT			M.avium
1216	CGAATCCTTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT				M.intracellulare
1258	CGAATCCTTTTAAGCCGGACTCAGTTCGGATTGGGGTCT				M.paratuberc.
1224	CGAATCCTTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT				M.scrofulaceum
1229	CGAATCCTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT				M.tuberculosis
1368	CGAATCCTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT				M.bovis
1279	CGAATCCTTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT				M.leprae
1226	CGAATCCTTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT				M.kansasii
1227	CGAATCCTTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT				M.gastri
1260	CGAATCCTTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT				M.gordonae
1221	CGAATCCTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT				M.marinum

	1330	1340	1350	1360	
1304	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.avium
1256	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.intracellulare
1298	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.paratuberc.
1264	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.scrofulaceum
1268	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.tuberculosis
1407	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.bovis
1319	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.leprae
1266	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.kansasii
1267	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.gastri
1300	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.gordonae
1260	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.marinum

Figure 5B

2550 | TTACGGCGGGCAGGACGAAAGACCCCGGGACCTTCACTA | 2589

2568 2569 |

Mavium 23S:

Figure 6

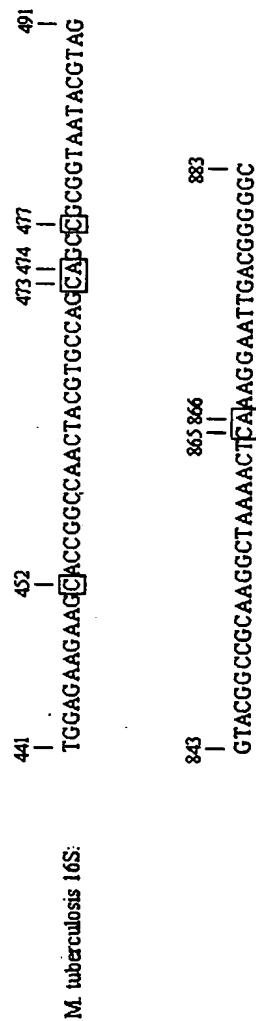


Figure 7